

REMARKS

The present application was filed on February 20, 2004 with claims 1-19. Claims 4-7, 10-12, 15, 16, 18 and 19 have been withdrawn. Claims 1, 8, 13, and 17 are the pending independent claims.

In the outstanding Office Action dated November 28, 2007, the Examiner: (i) rejected claims 1-3, 8, 9, 13, 14, and 17 under 35 U.S.C. §112, second paragraph; and (ii) rejected claims 1-3, 8, 9, 13, 14, and 17 under 35 U.S.C. §102(b) as being anticipated by U.S. Patent No. 5,706,498 to Fujimiya et al. (hereinafter “Fujimiya”).

Initially, Applicant very respectfully requests that the Examiner refrain from grouping the claim language of the claims together in future office actions when presenting the arguments for rejection. Applicant respectfully requests that the Examiner present the arguments claim by claim. By merging the claim language, it is very difficult for the Applicant to clearly understand and respond to the Examiner’s arguments with specificity.

With regard to the rejection of claims 1-3, 8, 9, 13, 14, and 17 under 35 U.S.C. §112, second paragraph, independent claims 1, 8, 13, and 17 have been amended to more clearly point out and distinctly claim the subject matter which the applicant regards as the invention. For example, Applicant has removed the wording “that may be bound to a target nucleotide.” Accordingly, withdrawal of the rejection of claims 1-3, 8, 9, 13, 14, and 17 under 35 U.S.C. §112 is therefore respectfully requested.

Applicant has also amended the independent claims to recite evaluating a binding possibility of the target nucleotide sequence data to the probe nucleotide sequence via a determination of whether the complementary sequence data of the probe nucleotide sequence is similar to a subsequence of the target nucleotide sequence data, wherein the evaluation is performed in descending order of edit distance of binding precision, further wherein edit distance is the number of times nucleotides of the subsequence are required to be adjusted to generate the complementary sequence data. Support for these amendments may be found in the specification at page 15, line 9, to page 16, line 11; and page 14, lines 1-18.

With regard to the rejection of claims 1-3, 8, 9, 13, 14 and 17 under 35 U.S.C. §102(b) as being anticipated by Fujimiya, Applicant initially notes that it is well-established law that a claim

is anticipated only if each and every element as set forth in the claim is found, either expressly or inherently described, in a single prior art reference. Verdegaal Bros. v. Union Oil Co. of California, 814 F.2d 628, 631, 2 U.S.P.Q.2d 1051, 1053 (Fed. Cir. 1987). Applicant asserts that the rejection based on Fujimiya does not meet this basic legal requirement.

Applicant asserts that Fujimiya fails to teach or suggest each and every element of the claims as amended. Fujimiya discloses a gene database retrieval system utilizing the sequence data of the bases of a gene from a gene database as target data and the sequence data of the bases as a key for retrieval. (Fujimiya, Abstract). More specifically, Fujimiya describes retrieving genes from a gene database by determining a degree of similarity between the target data (e.g., sequence data of the bases of a gene from the gene database) and key data (e.g., sequence data which is used as a key to retrieve gene information from the gene database). (Fujimiya, Abstract). Retrieving genes from a database does not anticipate screening nucleotide sequences as recited in the claims.

For instance, in contrast to the Examiner's argument, the target data and the key data disclosed by Fujimiya fails to anticipate the target nucleotide sequence data and complementary sequence data recited in independent claims 1, 8, 13, and 17. The complementary sequence data recited in the claims is generated from a probe nucleotide sequence. (Claim 1). Fujimiya does not disclose generating complementary sequence data from a probe nucleotide sequence. The Examiner argues that Fujimiya teaches determining a final sequence of bases by extracting a portion of the gene probe bound to a chromosome and therefore, Fujimiya teaches generating complementary sequence data from a probe sequence. (Office Action, pg. 4, lines 2-6). Applicant strongly disagrees. Fujimiya is describing gene probe analysis where a probe is used to locate a position in a chromosome where gene information is located. (Fujimiya, col. 2, lines 8-17). Fujimiya is simply stating that the final sequence of bases of a gene may be determined by extracting the portion of the gene probe bound to the chromosome. (Fujimiya, col. 2, lines 18-20). This does not teach generating complementary sequence data from a probe nucleotide sequence and storing the complementary sequence data as recited in the claims.

It follows that Fujimiya fails to teach evaluating a binding possibility of the target nucleotide sequence data to the probe nucleotide sequence via a determination of whether the

complementary sequence data of the probe nucleotide sequence is similar to a subsequence of the target nucleotide sequence data. Applicant first notes that Fujimiya is not evaluating a binding possibility of the nucleotide sequence data to the probe nucleotide sequence. Fujimiya simply searches for target data that matches the key data and presents the target data in the order of higher degrees of similarity (Fujimiya, col. 23, lines 26-32). In other words, Fujimiya is retrieving target data which best matches the key data (e.g., a gene retrieval system).

Further, when Fujimiya teaches the gene retrieval system, Fujimiya is not generating complementary sequence data of a probe nucleotide sequence and then using the complementary sequence data to determine if it is similar to a subsequence of the target nucleotide sequence in order to evaluate the binding possibility. In contrast to the Examiner's argument, Fujimiya does not disclose complementary sequence data.

The claims further recite that the evaluation of binding possibility is performed in descending order of edit distance of binding precision. An exemplary embodiment of edit distance is described in the specification at, for example, page 14, lines 1-10 with reference to figure 1(b). Edit distance is also recited in the claims as the number of times nucleotides of the subsequence are required to be adjusted to generate the complementary sequence data. (Claim 1). Fujimiya does not teach edit distance as recited in the claims. Furthermore, Fujimiya does not teach that the evaluation is performed in descending order of edit distance. Fujimiya is concerned with finding the target data which best matches the key data; therefore, Fujimiya searches for the best match first as opposed to the worst match first (e.g., descending order of edit distance).

Applicant respectfully requests that the Examiner consider the claims in their entirety and not lose sight of the subject matter of the recited claims. For example, claim 1 recites that the evaluation result of the evaluation process is used by a user in determining binding effectiveness and reliability of the probe nucleotide sequence to the target nucleotide sequence. Applicant believes that this language, at the very least, distinguishes the recited claims from Fujimiya. Fujimiya is not concerned with determining binding effectiveness and reliability of a probe nucleotide sequence to a target nucleotide sequence. Fujimiya simply retrieves genes from a gene database using a sequence as a key.

For at least these reasons, Fujimiya fails to anticipate independent claims 1, 8, 13, and 17. It follows that dependent claims 2, 3, 9, and 14 are patentable at least by virtue of their dependency from independent claims 1, 8, and 13 and also recite patentable subject matter in their own right. Accordingly, withdrawal of the §102(b) rejection of claims 1-3, 8, 9, 13, 14, and 17 is respectfully requested.

In view of the above amendments and remarks, Applicant believes that claims 1-19 are in condition for allowance, and respectfully request withdrawal of the §112 and §102(b) rejections.

Respectfully submitted,



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